

SEQUENCE LISTING

<110> Merck Patent GmbH

<120> Novel G-Protein coupled receptor

5

<130> HGRL101KDWS

<140>

<141>

10

<160> 2

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 474

<212> DNA

<213> Homo sapiens

20

<220>

<221> CDS

<222> (1)..(474)

<400> 1

25	gcc cag att tat tca gtg gca att ttt ctt ggt att aat ttg gcc gca	48
	Ala Gln Ile Tyr Ser Val Ala Ile Phe Leu Gly Ile Asn Leu Ala Ala	
	1 5 10 15	
30	ttt atc atc ata gtt ttt tcc tat gga agc atg ttt tat agt gtt cat	96
	Phe Ile Ile Ile Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His	
	20 25 30	
35	caa agt gcc ata aca gca act gaa ata cgg aat caa gtt aaa aaa gag	144
	Gln Ser Ala Ile Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu	
	35 40 45	
40	atg atc ctt gcc aaa cgt ttt ttc ttt ata gta ttt act gat gca tta	192
	Met Ile Leu Ala Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu	
	50 55 60	
45	tgc tgg ata ccc att ttt gta gcg aaa cct ctt tca ctg ctt cag gta	240
	Cys Trp Ile Pro Ile Phe Val Ala Lys Pro Leu Ser Leu Leu Gln Val	
	65 70 75 80	
50	gaa ata cca ggt acc ata acc tct tgg gta gtg att ggt tat tct gcc	288
	Glu Ile Pro Gly Thr Ile Thr Ser Trp Val Val Ile Gly Tyr Ser Ala	
	85 90 95	
55	att aac agt gct ttg aac cca att ctc tat act ctg acc aca aga cca	336
	Ile Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro	
	100 105 110	
60	ttt aaa gaa atg att cat cgg ttt tgg cat aac tac aga caa aga aaa	384
	Phe Lys Glu Met Ile His Arg Phe Trp His Asn Tyr Arg Gln Arg Lys	
	115 120 125	
65	tct atg gac agc aaa ggt atc aga aaa cat atg ctc cat cat tca tct	432
	Ser Met Asp Ser Lys Gly Ile Arg Lys His Met Leu His His Ser Ser	
	130 135 140	
70	ggg ggg aaa tgt ggc cac tgc agg aga tgc cac ctg agt taa	474

Gly Gly Lys Cys Gly His Cys Arg Arg Cys His Leu Ser
145 150 155

5 <210> 2
<211> 157
<212> PRT
<213> Homo sapiens

10 <400> 2
Ala Gln Ile Tyr Ser Val Ala Ile Phe Leu Gly Ile Asn Leu Ala Ala
1 5 10 15
Phe Ile Ile Ile Val Phe Ser Tyr Gly Ser Met Phe Tyr Ser Val His
20 25 30
15 Gln Ser Ala Ile Thr Ala Thr Glu Ile Arg Asn Gln Val Lys Lys Glu
35 40 45
Met Ile Leu Ala Lys Arg Phe Phe Phe Ile Val Phe Thr Asp Ala Leu
50 55 60
Cys Trp Ile Pro Ile Phe Val Ala Lys Pro Leu Ser Leu Leu Gln Val
20 65 70 75 80
Glu Ile Pro Gly Thr Ile Thr Ser Trp Val Val Ile Gly Tyr Ser Ala
85 90 95
Ile Asn Ser Ala Leu Asn Pro Ile Leu Tyr Thr Leu Thr Thr Arg Pro
100 105 110
25 Phe Lys Glu Met Ile His Arg Phe Trp His Asn Tyr Arg Gln Arg Lys
115 120 125
Ser Met Asp Ser Lys Gly Ile Arg Lys His Met Leu His His Ser Ser
130 135 140
Gly Gly Lys Cys Gly His Cys Arg Arg Cys His Leu Ser
30 145 150 155